



Description of Transcription Factor Binding Sites Present on Promoters						
Isolated From SignalTag Sequences						
Promoter sequence P13H2 (546 bp):						
Matrix	Position	Orientation	Score	Length	Sequence	SEQ ID NO:
CMYB_01	-502	+	0.983	9	TGTCAGTTG	19336
MYOD_Q6	-501	-	0.961	10	CCCAACTGAC	19337
S8_01	-444	-	0.960	11	AATAGAATTAG	19338
S8_01	-425	+	0.966	11	AACTAAATTAG	19339
DELTAEF1_01	-390	-	0.960	11	GCACACCTCAG	19340
GATA_C	-364	-	0.964	11	AGATAAAATCCA	19341
CMYB_01	-349	+	0.958	9	CTTCAGTTG	19342
GATA1_02	-343	+	0.959	14	TTGTAGATAGGACA	19343
GATA_C	-339	+	0.953	11	AGATAGGACAT	19344
TAL1ALPHAE47_01	-235	+	0.973	16	CATAACAGATGGTAAG	19345
TAL1BETAE47_01	-235	+	0.983	16	CATAACAGATGGTAAG	19345
TAL1BETAIF2_01	-235	+	0.978	16	CATAACAGATGGTAAG	19345
MYOD_Q6	-232	-	0.954	10	ACCATCTGTT	19346
GATA1_04	-217	-	0.953	13	TCAAGATAAAAGTA	19347
IK1_01	-126	+	0.963	13	AGTTGGGAATTCC	19348
IK2_01	-126	+	0.985	12	AGTTGGGAATTCC	19349
CREL_01	-123	+	0.962	10	TGGGAATTCC	19350
GATA1_02	-96	+	0.950	14	TCAGTGTATGGCA	19351
SRY_02	-41	-	0.951	12	AAAACAAAACA	19352
E2F_02	-33	+	0.957	8	TTTAGCGC	19353
MZF1_01	-5	-	0.975	8	TGAGGGGA	19354
Promoter sequence P15B4 (861bp) :						
Matrix	Position	Orientation	Score	Length	Sequence	SEQ ID NO:
NFY_Q6	-748	-	0.956	11	GGACCAATCAT	19355
MZF1_01	-738	+	0.962	8	CCTGGGGA	19356
CMYB_01	-684	+	0.994	9	TGACCGTTG	19357
VMYB_02	-682	-	0.985	9	TCCAACGGT	19358
STAT_01	-673	+	0.968	9	TTCCCTGGAA	19359
STAT_01	-673	-	0.951	9	TTCCAGGAA	19360
MZF1_01	-556	-	0.956	8	TTGGGGGA	19361
IK2_01	-451	+	0.965	12	GAATGGGATTTTC	19362
MZF1_01	-424	+	0.986	8	AGAGGGGA	19363
SRY_02	-398	-	0.955	12	AAAACAAAACA	19364
MZF1_01	-216	+	0.960	8	GAAGGGGA	19365
MYOD_Q6	-190	+	0.981	10	AGCATCTGCC	19366
DELTAEF1_01	-176	+	0.958	11	TCCCACCTTCC	19367
S8_01	5	-	0.992	11	GAGGCAATTAT	19368
MZF1_01	16	-	0.986	8	AGAGGGGA	19369
Promoter sequence P29B6 (555 bp) :						
Matrix	Position	Orientation	Score	Length	Sequence	SEQ ID NO:
ARNT_01	-311	+	0.964	16	GGACTCACGTGCTGCT	19370
NMYC_01	-309	+	0.965	12	ACTCACGTGCTG	19371
USF_01	-309	+	0.985	12	ACTCACGTGCTG	19371
USF_01	-309	-	0.985	12	CAGCACGTGAGT	19372
NMYC_01	-309	-	0.956	12	CAGCACGTGAGT	19372
MYCMAX_02	-309	-	0.972	12	CAGCACGTGAGT	19372
USF_C	-307	+	0.997	8	TCACGTGC	19373
USF_C	-307	-	0.991	8	GCACGTGA	19374
MZF1_01	-292	-	0.968	8	CATGGGGA	19375
ELK1_02	-105	+	0.963	14	CTCTCCGGAAGCCT	19376
CETS1P54_01	-102	+	0.974	10	TCCGGAAGCC	19377
AP1_Q4	-42	-	0.963	11	AGTGAAGAAC	19378
AP1FJ_Q2	-42	-	0.961	11	AGTGAAGAAC	19378
PADS_C	45	+	1.000	9	TGTGGTCTC	19379

Figure 5



8/10

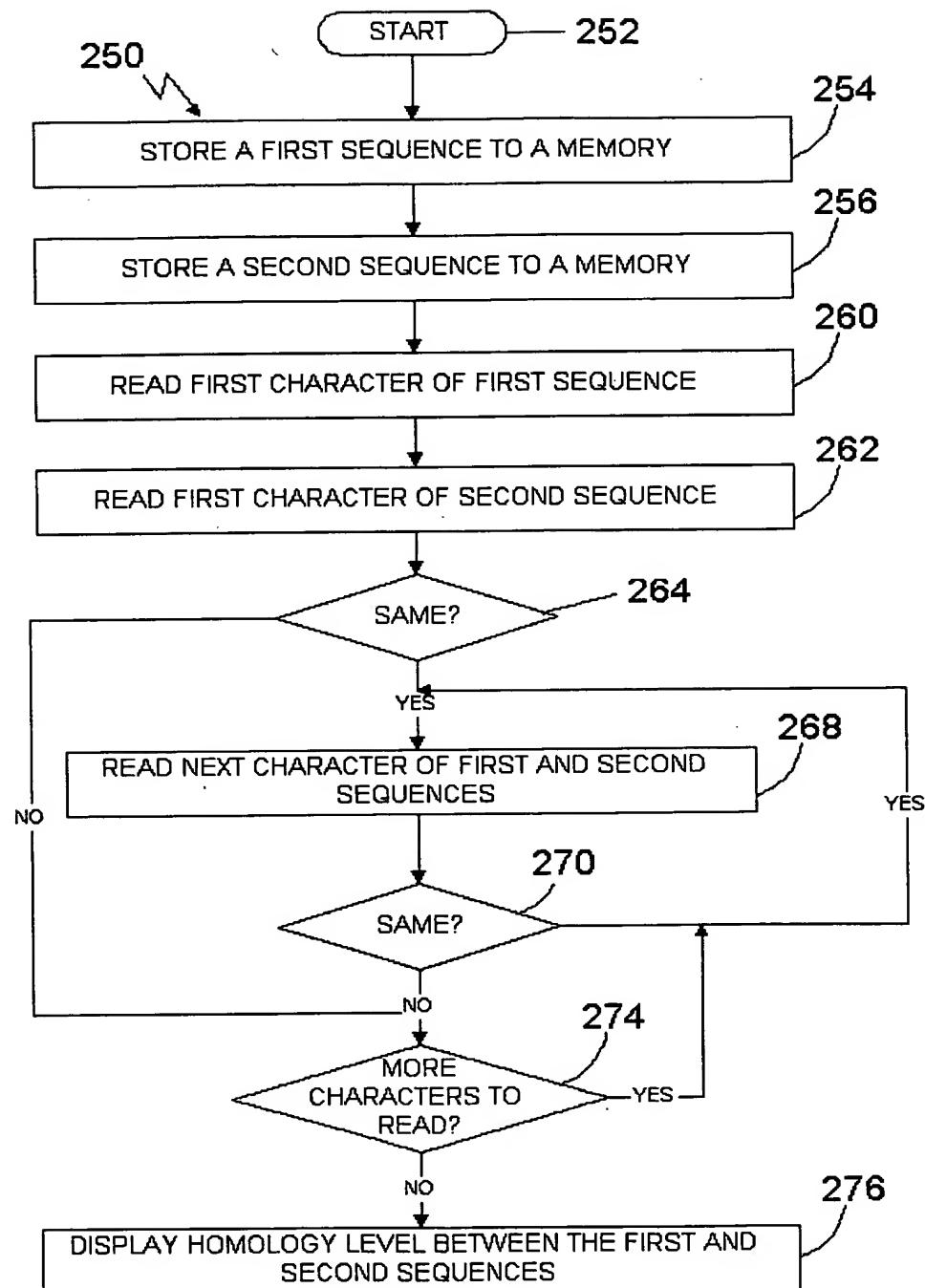


FIGURE 8